

FIG. 1

1 MNDPNS CVDNATV CSGA SC - - - VVPESNFNNI LSV LSTV ISBT
 1 MRA - - NC - SSSSAC PAN SSEEELPVGLEVHGN LELV FTVV TCH230

38 L T I L L A L V M F S M G C N V E I K K F L G H I K R P W G I C V G F L C Q F G ISBT
 38 S T V M M G L L M F S L G C S V E I R K L W S H I R R P W G I A V G L L C Q F G TCH230

78 I M P L T G F I L S V A F D I L P L Q A V V V L I I G C C P G G T A S N I L A Y ISBT
 78 L M P F T A Y L L A I S F S L K P V Q A I A V L I M G C C P G G T I S N I F T F TCH230

118 W V D G D M D L S V S M T T C S T L L A L G M M P L C L L I Y T K M W V D S G S ISBT
 118 W V D G D M D L S I S M T T C S T V A A L G M M P L C I Y L Y T W S W S L Q Q N TCH230

158 I V I P Y D N I G T S L V A L V V P V S I G M F V N H K W P Q K A K I I L K I G ISBT
 158 L T I P Y Q N I G I T L V C L T I P V A P G V Y V N Y R W P K Q S K I I L K I G TCH230

198 S I A G A I L I V L I A V V G G I L Y Q S A W I I A P K L W I I G T I F P V A G ISBT
 198 A V V G G V L L L V V A V A G V V L A K G S W N S D I T L L T I S F I F P L I G TCH230

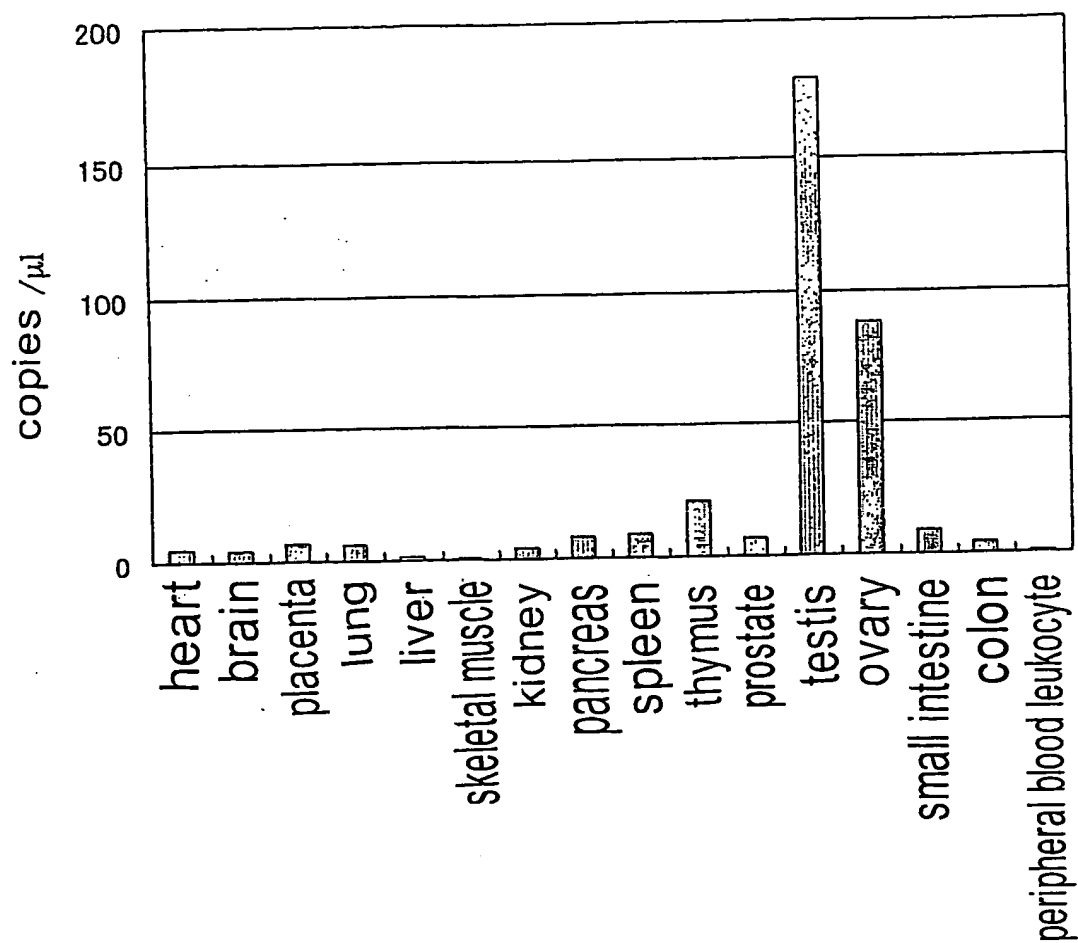
238 Y S L G F L L A R I A G L P W Y R C R T V A F E T G M Q N T Q L C S T I V Q L S ISBT
 238 H V T G F L L A L F T H Q S W Q R C R T I S L E T G A Q N I Q M C I T M L Q L S TCH230

278 F T P E E L N V V P T F P L I Y S I F Q L A F A A I F L G F Y V A Y K K C - - - ISBT
 278 F T A E E L V Q M L S F P L A Y G L F Q L I D G P L I V A A Y Q T Y K R R L K N TCH230

315 - H G K N K A - - - E I P E S K E N G T E P E S S F Y - - - K A N G G F Q P D E ISBT
 318 K H G K K N S G C T E V C H T R K S T S S R E T N A F L E V N E E G A I T P G P TCH230

348 - - - - - K ISBT
 358 P G P M D C H R A L E P V G H I T S C E TCH230

FIG. 2



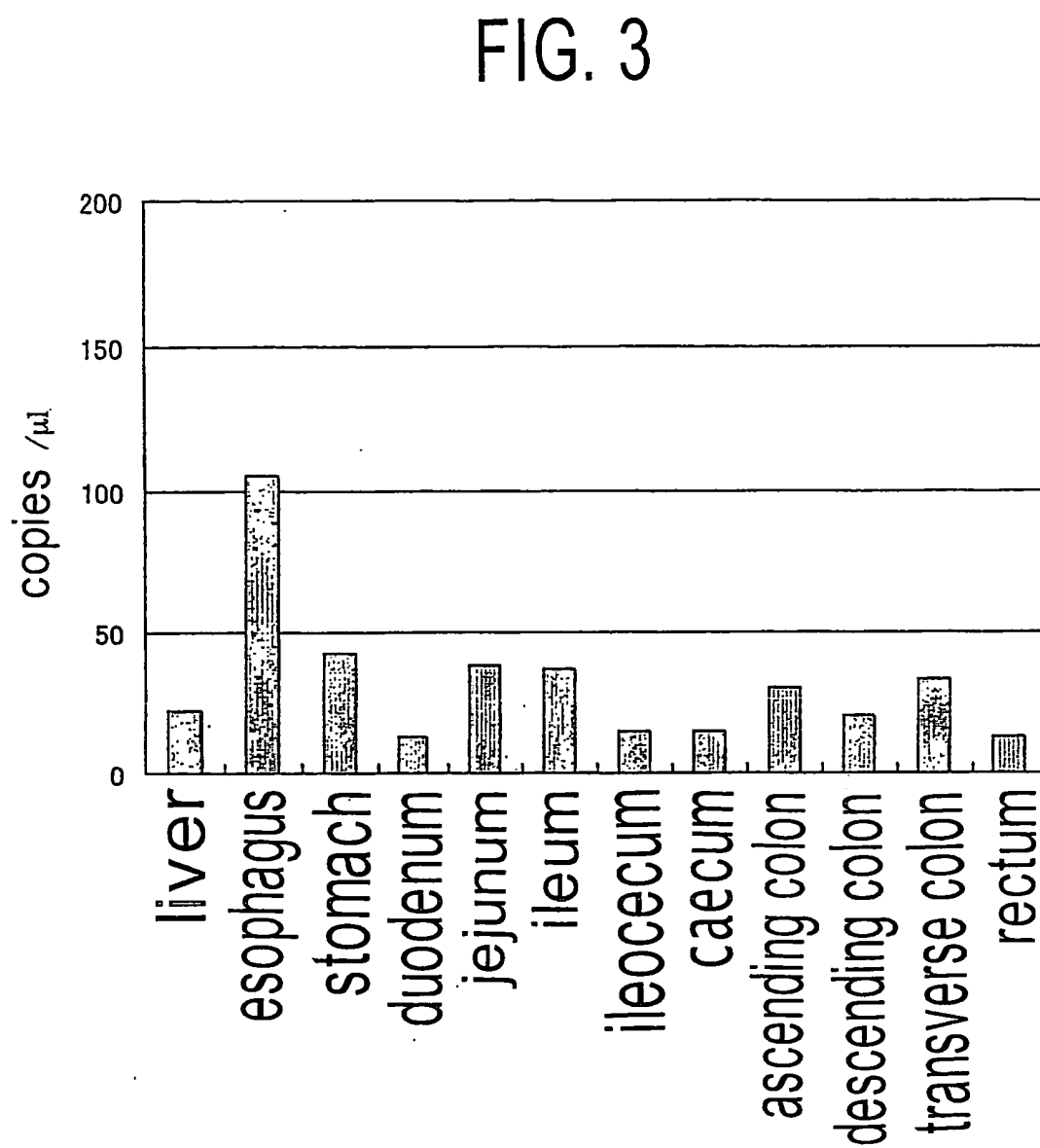


FIG. 4

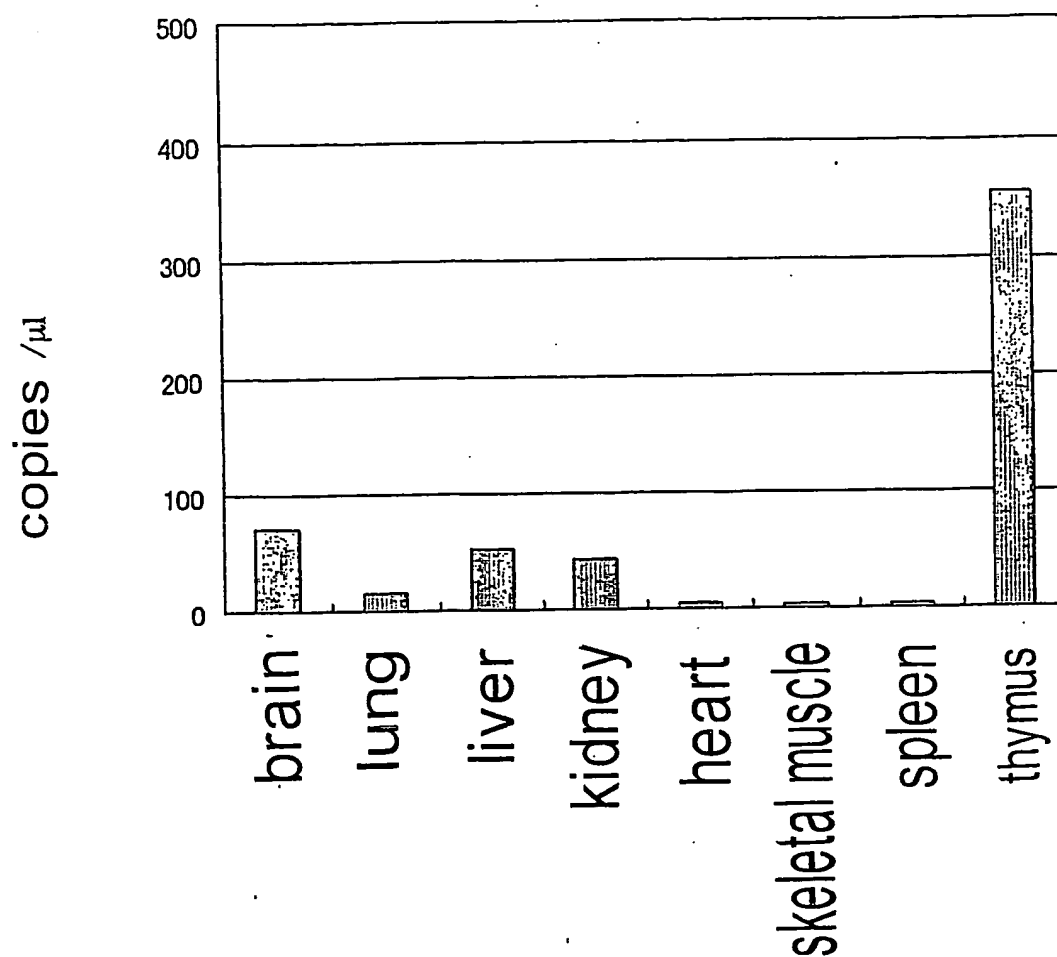


FIG. 5

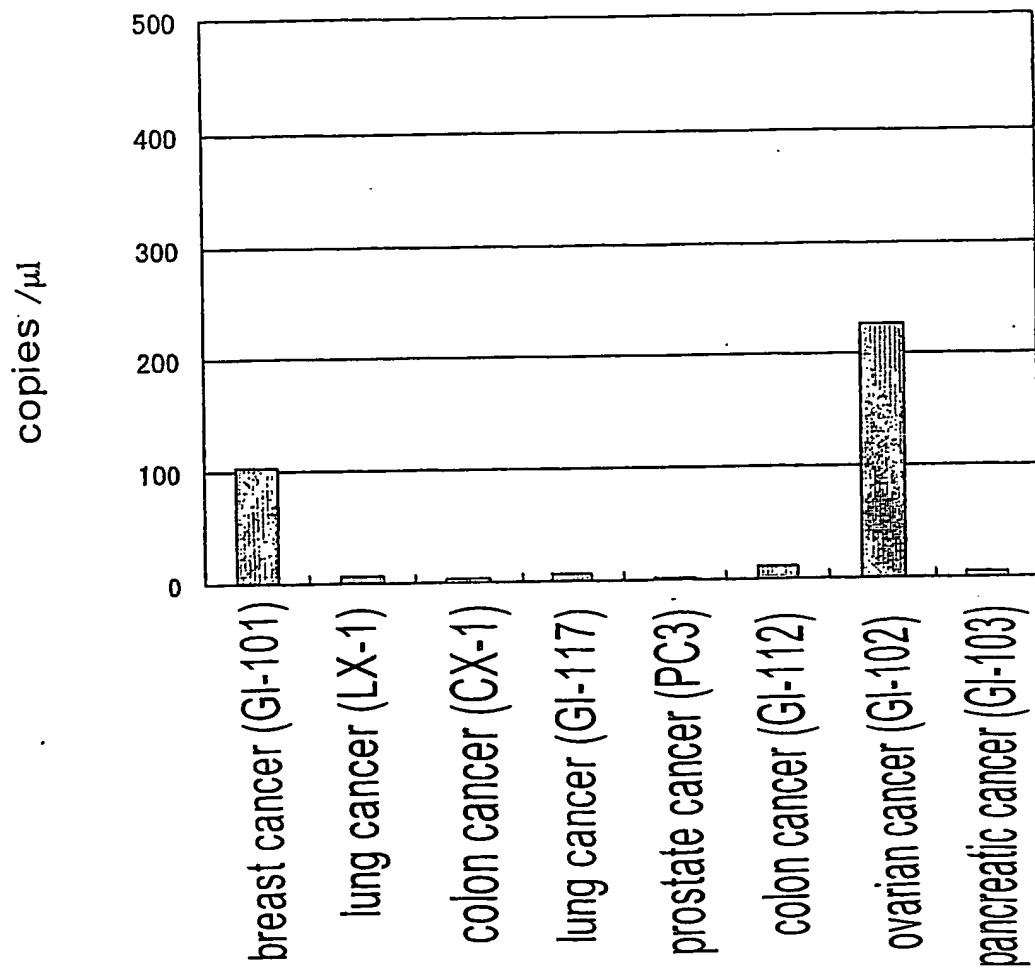


FIG. 6

		TM1		
TCH234	MAIQMFVYSPNCT-----LLIVAESEASSDLNESANSTAYASNPWFARASSE-----			54
ratNHE4	MGEAMLRAPSSKWT-----LLIMVLTLEASSYVNESSPGQOTPDARFAASSSD-----			54
humanNHE2	MEH-----LGNMRSLRAPLPMLLLQVAGPVGADAEITLLNAPRAMGTSSSPPEPASVVAPGTTLFE			65
		TM2	TM3	
TCH234	EGISVFELDYDYVQIPYEVTLWILLASLAKIGFHLHYRLEGLMPESCLLILVGLVGGIIFGTDHKSPPV			124
ratNHE4	ERISVFELDYDYVQIPYEVTLWILLASLAKIGFHLHYRLEGLMPESCLLILVGLVGGIIFGTDHKSPPV			124
humanNHE2	SRLPVEITLDYPHVQIIFETLWILLASLAKIGFHLHYRLEGLMPESCLLILVGLVGGIIFGTDHKSPPV			135
		TM4	TM5	
TCH234	MDSSIFLYLLPPIVLEGGYFMPTRPFFENIGSILWVAVLGALINALGIGLSLYLICQVKAFLGLGVNLI			194
ratNHE4	MDSSIFLYLLPPIVLEGGYFMPTRPFFENIGSILWVAVLGALINALGIGLSLYLICQVKAFLGLGVNLI			194
humanNHE2	MKTDPVFLYLLPPIVLDAGYFMPTRPFFENIGSILWVAVLGALINALGIGLSLYLICQVKAFLGLGVNLI			205
		TM6	TM7	
TCH234	QNLLFGSLISAVDPVAVLAVFEEARVNEQLYMMIFGEALLNDGIVTVLYNLIAFTKMHKFEDIEVDII			264
ratNHE4	QNLLFGSLISAVDPVAVLAVFEEARVNEQLYMMIFGEALLNDGIVTVLYNLIAFTKMHKFEDIEVDII			264
humanNHE2	QNLLFGSLISAVDPVAVLAVFENIHVNEQLYILVFGESLLNDAVTVVLYNLIAFTKMHKFEDIEVDII			272
		TM8	TM9	
TCH234	AGCAREFIVGLGGVLPGLVFGFISAFITRPTONISAIPLIVFMPFSYLSYLAETLYLSGILAITACAVT			334
ratNHE4	AGCAREFIVGLGGVLPGLVFGFISAFITRPTONISAIPLIVFMPFSYLSYLAETLYLSGILAITACAVT			334
humanNHE2	AGINNEFVVGIGGVILGIFLGFIAFTTRPTONIRVIEPLIVFVLSYLSYLAETLYLSGILAITACAVT			342
		TM10	TM11	
TCH234	MKKYVEENVSTSYTTIKYFMKMLSSVSETLIFIPMGVSTVGKNHEWNWAFVCTLAFCQIWRRAISVETL			404
ratNHE4	MKKYVEENVSTSYTTIKYFMKMLSSVSETLIFIPMGVSTVGKNHEWNWAFVCTLAFCQIWRRAISVETL			404
humanNHE2	MKKYVEENVSTSYTTIKYFMKMLSSVSETLIFIPMGVSTVGKNHEWNWAFVCTLAFCQIWRRAISVETL			412
		TM12	TM13	
TCH234	FYISNQFRTFFPSIKDCLIFYSVGRGAGSFLAFLPLISLFRKRMFVTATLVVYFTVFIQGITVGPV			474
ratNHE4	FYVSNQFRTFFPSIKDCLIFYSVGRGAGSFLAFLPLISLFRKRMFVTATLVVYFTVFIQGITVGPV			474
humanNHE2	TOVINRFRITELTFKDCPIIANGGLRGATCFANVFLHAAVFRKKLEITAIIVVFFTVFVILGITIRPI			482
TCH234	VRYLDVKKTNNKE-SINEELHIRLMDHLKAGIEDVCGHWSHYQVRDKFKKFDHRYLRKILIRNPKSSI			543
ratNHE4	VRYLDVKKTNNKE-SINEELHIRLMDHLKAGIEDVCGHWSHYQVRDKFKKFDHRYLRKILIRNPKSSI			543
humanNHE2	VEPLDVKRSNKKQAVSEEIYCRIFDVHTGIEDVCGHWSHYQVRDKFKKFDHRYLRKILIRNPKSSI			552
TCH234	VSLEYKLEMKQAIENVETGILSSVSPFTHHQAQRIQGIKRLSPEDVESIRDILTSNMYQVRQRTLSYNKY			613
ratNHE4	VSLEYKLEMKQAIEMAETGLSSVSPFTHHQAQRIQGIKRLSPEDVESMRDILTRNMYQVRQRTLSYNKY			613
humanNHE2	VSLEYKLEMKQAIEMAETGMISTVPTFASLNDCEEKIRKVTSSSETDEIRRELSRNLYQIRQRTLSYNKH			622
TCH234	NLKPQTSEKQAKEILIRRONTLRESMRKQHSPLWPKPAGTKNIRYLSYFYGNPQSG-RDTRANGFSDD			682
ratNHE4	NLKPQTSEKQAKEILIRRONTLRESLRKGOSLPWPKPAGTKNIRYLSYFYGNPQSG-RGARAN-----ES			678
humanNHE2	SETADTSERQAKEILIRRRHSLRESIRKDSINREHRNSTSTSYLSLEKNTKLEKLOKRFTISIAIGN			692
TCH234	SSDPGSPSIFSAQSRIGSLQKQEQEILIMKSLERGRKAFSPGYQRNTSQEYFG-----			739
ratNHE4	TGNE-----CWL-----LH-----FT-----			690
humanNHE2	SSSDADAGIT-----VLNLQPR-RRRFLHEQFSKKSQSYKMEWKNEVDVDSGRDMPSTPTPHSREK			756
TCH234	VERRVLRPKFIPHAVDEEGSGGE-SEGKASLVEVRSMTDGHGSDHHRSHSPLQKK			798
ratNHE4	-----LCRPM-----VEKINGPG-----GOETQPRLLCRNLN			717
humanNHE2	TQTSGLOQPLLSKDQSGSREDSLTEGIPPKPPPRLVRRSEPCSRKARFGSEK-----P			812

FIG. 7

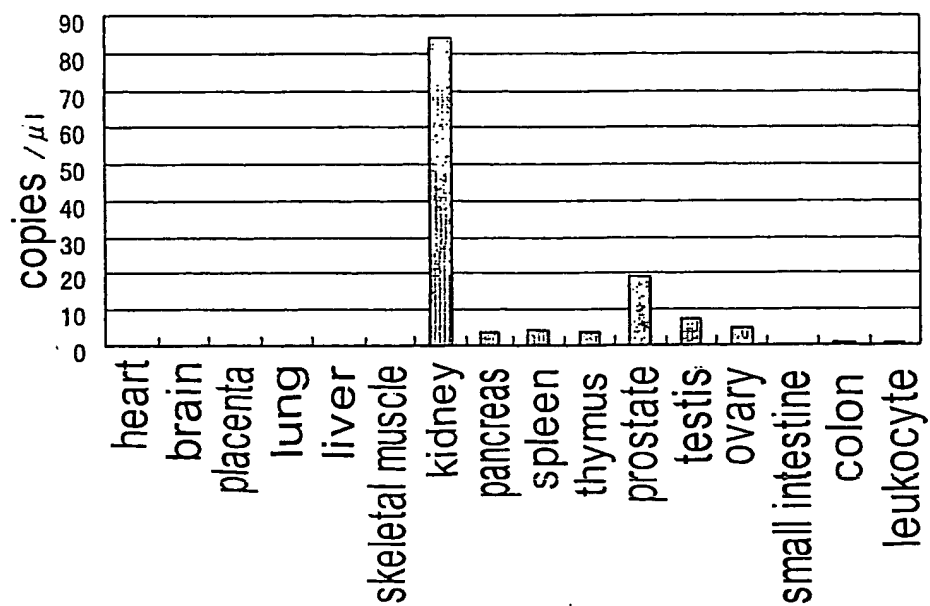


FIG. 8

[illegible]

400	F K K C S I A G V T Y G H F P E L A R E Q S S D D F - C - - - R M T S C T N D S C D F N D P R R L L K N I E D Q H P T A	MATP8A2 ATP8A1 TCH212
421	F K K C T I A G V A Y G H V P E - - - - P E D Y G C S P D E W Q N S Q F G D E K T F S D S S L L E N L Q N N H P T A	ATP8A1 TCH212
400	F K K C S I A G V T Y G H F P E L A R E P S S D D F - C - - - R M P P P C S D S C D F D D P R L L K N I E D R H P T A	ATP8A1 TCH212
455	P C I Q E F L T L L A V C H T V V P E K D G D E I I Y Q A S S P D E A A L V K G A K K L G F V F T G R T P Y S V I I E A	MATP8A2 ATP8A1 TCH212
475	P I Y C E F L T M M A V C H T A V P E R E G D K I I Y Q A A S P D E G A L V R A A K Q L L N F V F T G R T P D S V I I D S	ATP8A1 TCH212
455	P C I Q E F L T L L A V C H T V V P E K D G D N I I Y Q A S S P D E A A L V K G A K K L G F V F T A R T P F S V I I E A	ATP8A1 TCH212
515	M G Q E Q T F G I L N V L E F S S D R K R M S V I V R L P S C Q L R L Y C K G A D N V I F E R L S K D S K Y M E E T L C	MATP8A2 ATP8A1 TCH212
535	L G Q E E R Y E L L N V L E F T S A R K R M S V I V R T P S G K L R L Y C K G A D T V I Y D R L A E T S K Y K E I T L K	ATP8A1 TCH212
515	M G Q E Q T F G I L N V L E F S S D R K R M S V I V R T P S G R L R L Y C K G A D N V I F E R L S K D S K Y M E E T L C	ATP8A1 TCH212
575	H L E Y F A T E G L R T L C V A Y A D L S E N E Y E E W L K V Y Q E A S I I L K D R A Q R L E E C Y E I I E K N L L L	MATP8A2 ATP8A1 TCH212
595	H L E Q F A T E G L R T L C F A V A E I S E S D F Q E W R A V Y Q R A S T S V Q N R L L K L E E S Y E L I E K N L Q L L	ATP8A1 TCH212
575	H L E Y F A T E G L R T L C V A Y A D L S E N E Y E E W L K V Y Q E A S T I L K D R A Q R L E E C Y E I I E K N L L L	ATP8A1 TCH212
635	G A T A I E D R L Q A G V P E T I A T L L K A E I K I W V L T G D K Q E T A I N I G Y S C R L V S Q N M A L I L L K E D	MATP8A2 ATP8A1 TCH212
655	G A T A I E D K L Q D Q V P E T I E T L M K A D I K I W I L T G D K Q E T A I N I G H S C K L L K K N M G M I V I N E G	ATP8A1 TCH212
635	G A T A I E D R L Q A G V P E T I A T L L K A E I K I W V L T G D K Q E T A I N I G Y S C R L V S Q N M A L I L L K E D	MATP8A2 ATP8A1 TCH212
695	S L D A T R A A I T Q H C T D L G N L L G K E N D V A L I I D G H T L K Y A L S F E V R R S F L D L A L S C K A V I C C	MATP8A2 ATP8A1 TCH212
715	S L D G T R E T L S R H C T T L G D A L L R K E N D F A L I I D G K T L K Y A L T F G V R Q Y F L D L A L S C K A V I C C	ATP8A1 TCH212
695	S L D A T R A A I T Q H C T D L G N L L G K E N D V A L I I D G H T L K Y A L S F E V R R S F L D L A L S C K A V I C C	MATP8A2 ATP8A1 TCH212
755	R V S P L Q K S E I V D V V K K R V K A I T L A I G D G A N D V G M I Q T A H V G V G I S G N E G M Q A T N N S D Y A I	MATP8A2 ATP8A1 TCH212
775	R V S P L Q K S E V V E M V K K Q V K V V T L A I G D G A N D V S M I Q T A H V G V G I S G N E G L Q A A N S S D Y S I	ATP8A1 TCH212
755	R V S P L O K S E I V D V V K K R V K A I T L A I G D G A N D V G M I Q T A H V G V G I S G N E G M Q A T N N S D Y A I	MATP8A2 ATP8A1 TCH212

FIG. 10

815	AQFSYL	EKLL	LVHGAW	SYNRV	TKCILYCFYKN	VVLYII	ELWF	AFVNGFS	QILFER	WCIG	mATP8A2
835	AQFKYL	KNLL	MIHGAW	NYNRV	SKCILYCFYKN	IVLYII	ELWF	AFVNGFS	QILFER	WCIG	ATP8A1
815	AQFSYL	EKLL	LVHGAW	SYNRV	TKCILYCFYKN	VVLYII	ELWF	AFVNGFS	QILFER	WCIG	TCH212
TM6											
875	LYNV	IFTAL	PPFT	TLGIFERS	C	TQES	MLRFR	QYRIT	QNAEG	FN	mATP8A2
895	LYNV	MTAM	PPFT	TLGIFERS	C	TKEN	MLRFR	QYKTS	QNALD	FN	ATP8A1
875	LYNV	IFTAL	PPFT	TLGIFERS	C	TQES	MLRFR	QYKIT	QNGEG	FN	TCH212
TM8											
935	LFWV	PMKAL	EHD	TPVTS	G	HATD	YLFV	GNIV	VTV	CL	mATP8A2
955	LFWV	PMKAL	QYGT	AFGNG	KTS	DYLL	GNIV	VTV	CL	KAG	ATP8A1
935	LFWV	PMKAL	EHD	TPVTS	G	HATD	YLFV	GNIV	VTV	CL	TCH212
TM9											
995	MLIW	LVFG	VYST	INPT	TI	PIA	PD	MKG	QA	TM	mATP8A2
1015	IALL	VVFG	IYSS	LWPA	I	PMAP	DM	SGE	AAM	LFSS	ATP8A1
995	MLTW	LVFG	IYSS	INPT	TI	PIA	PD	MKG	QA	TM	TCH212
TM10											
1055	CKKT	LEEV	QELE	ETKS	RV	MG	KAM	L	RDS	NG	mATP8A2
1075	TAFT	KTLL	VDE	VQELE	ETKS	QD	PG	AV	VL	- - -	ATP8A1
1055	CKKT	LEEV	QELE	ETKS	RV	MG	KAM	L	RDS	NG	TCH212
TM11											
1115	VSHG	YAFS	QEE	HGA	V	TQEE	IV	RAY	DT	TK	mATP8A2
1131	LHGY	AFS	QDE	NG	I	V	SQSE	IV	RAY	DT	ATP8A1
1115	VPHG	YAFS	QEE	HGA	V	TQEE	IV	RAY	DT	TK	TCH212

FIG. 11

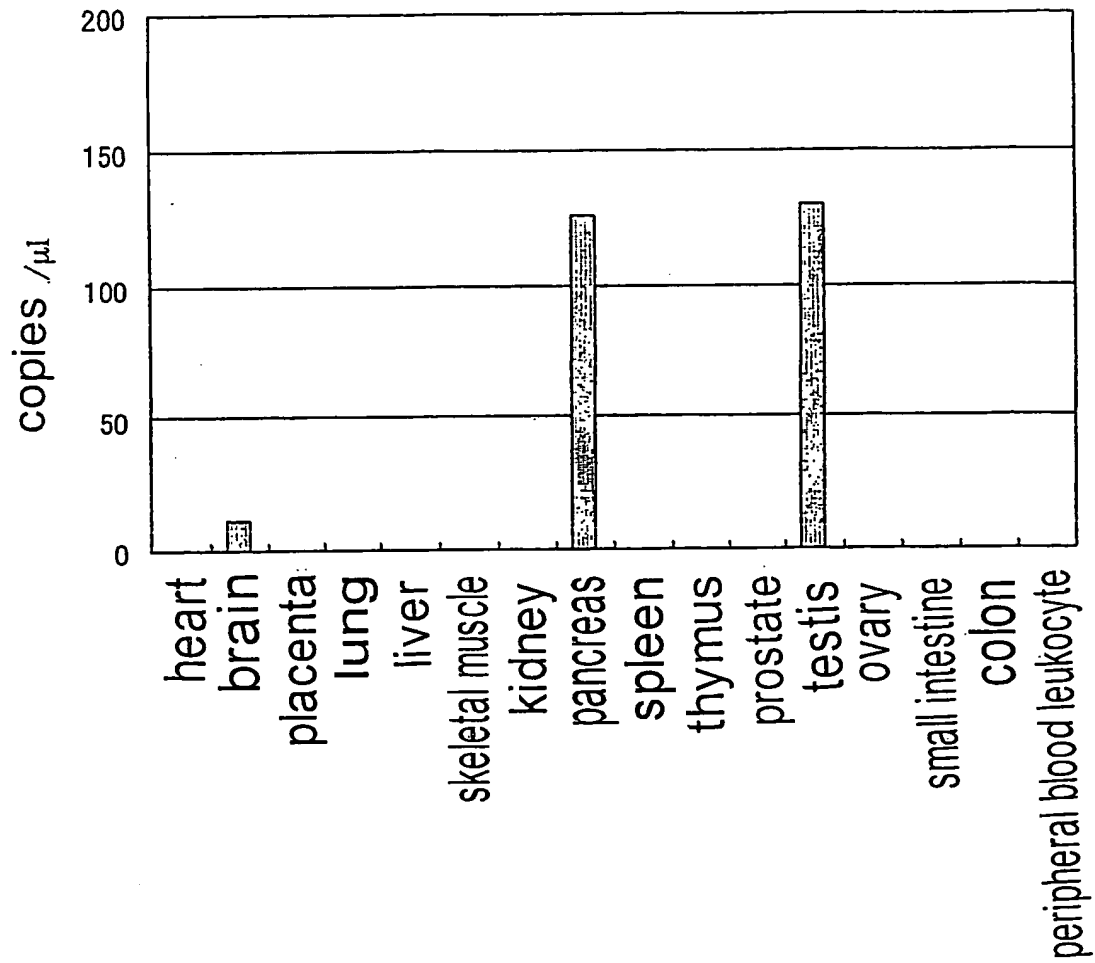


FIG. 12

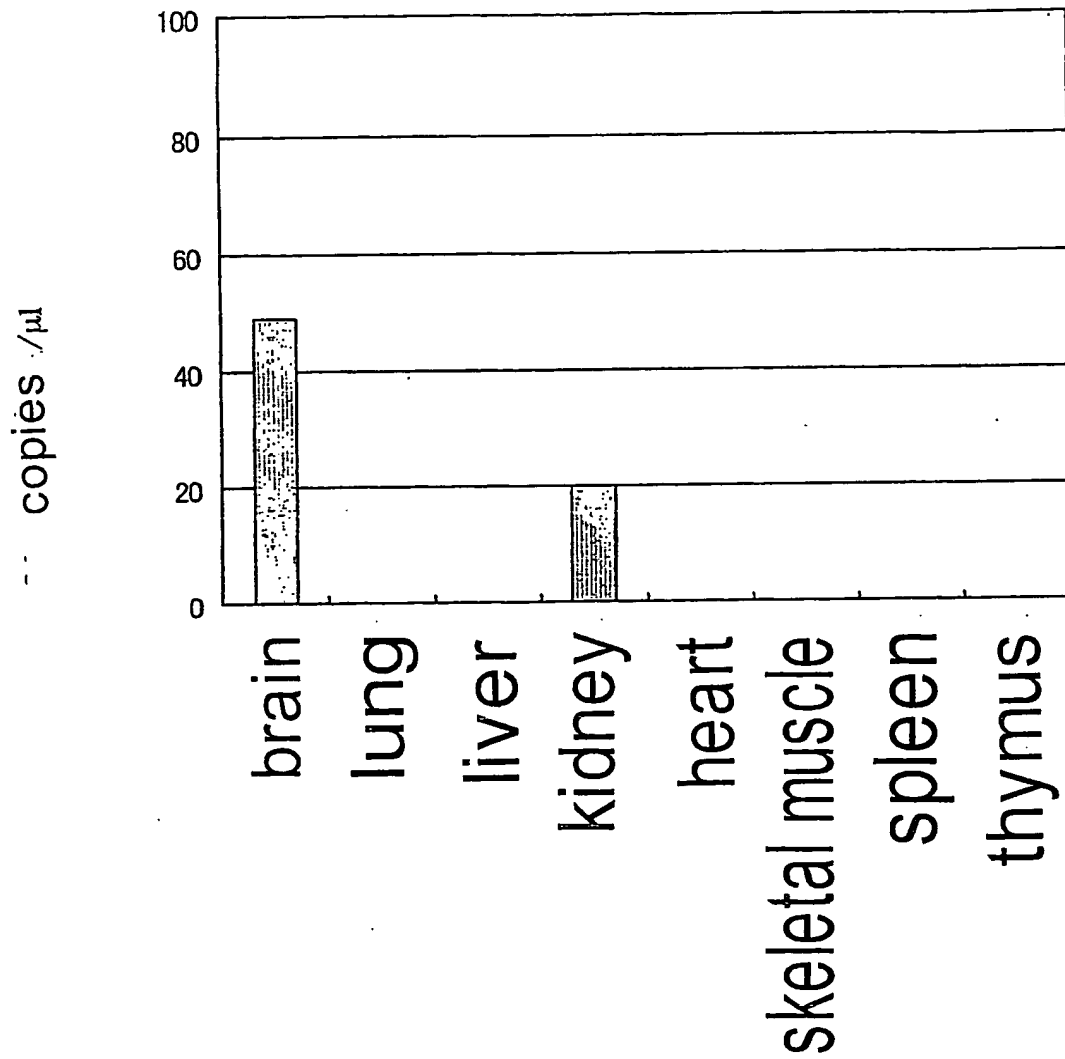


FIG. 13

1 M K X W S S T D L G A A A D P L Q K D T C P D P L D G D P N S R P P P A K P O L S T A K S R T R hVR1
 1 M K A H P K E M V P L N G K R V A A P S - - - - - G N P A V L P E K R P A E I T P T K K S A H TCH200

 49 L F - - - - - G K G D S E E A F P V D C P H E E G E L D S C P T I T V S P V I T I Q R P G hVR1
 43 F F L E I E G F E P N P T V A K T S P P V F S K P M D S N I R Q C I S G N C D D M D S P Q S P Q TCH200

 89 D G P T G A R L L S Q D S V A S T E K T L R L Y D R R - - S I F E A V A Q N N C Q D L E S L hVR1
 91 D D V T E T P S N P N S P S A Q L A K E E Q R R K K R R L K K R I F A A V S E G C V E E L V E L TCH200

 134 L L F L Q K - - S K K H L T D - - - - - N E F K D P E T G K T C L L K A M L N L H D G Q N T T hVR1
 139 L V E L Q E L C R R R H D E D V P D F L M H K L T A S D T G K T C L M K A L L N I N P N T K E I TCH200

 174 I P L L L E I A R Q T D S L K E L V N A S Y T D S Y Y K G Q T A L H I A I E R R N M A L V T L L hVR1
 187 V R I L L A F A E E N D I L G R F I N A E Y T E E A Y E G Q T A L N I A I E R R Q G D I A A L TCH200

 222 V E N G A D V Q A A A H G D F F K K T K G R P G F Y F G E L P L S L A A C T N Q L G I V K F L L hVR1
 235 I A A G A D V N A H A K G A F P N P K Y Q H E G F Y F G E T P L A L A A C T N Q P E I V Q L L M TCH200

 270 Q N S W Q T A D I S A R D S V G N T V L H A L V E V A D N T A D N T K F V T S M Y N E I L I L G hVR1
 283 E H - - E Q T D I T S R D S R G N N I L H A L V T V A E D F K T Q N D F V K R M Y D M I L L R S TCH200

 318 A K L H P T L K L E E L T N K K G M M P L A L A A G T G K I G V L A Y I L Q R E I Q E P E C R H hVR1
 329 G N W E - - - L E T T R N N D G L T P L Q L A A K M G K A E I L K Y I L S R E I K E K R L R S TCH200

 366 L S R K F T E W A Y G P V H S S L Y D L S C I D T C E K N S V L E V I A Y S S S E T P N R H D M hVR1
 373 L S R K F T D W A Y G P V S S S L Y D L T N V D T T D N S V L E I T V Y N T N I D - N R H E M TCH200

 414 L L V E P L N R L L Q D K W D R F V K R I F Y F N F L V Y C L Y M I I F T M A A Y Y R P V D G L hVR1
 420 L T L E P L H T L L H M K W K K F A K H M F F L S F C F Y F F Y N I T L T L S Y Y R P R E E - TCH200

 462 P P F K M E K T G D Y F R V T G E I - - L S V L G G V Y F F F - - - - - R G I Q Y F L Q R hVR1
 467 - - - - - E A I P H P L A L T H K M G W L Q L L G R M F V L I W A M C I S V K E G I A I F L L R TCH200

 500 R P S M K T L F V D S Y S E M L F F L Q S L F M L A T V V L Y P S H L K E Y V A S M V F S L A L hVR1
 510 P S D L Q S I L S D A W F H F V F F I Q A V L V I L S V F L Y L F A Y K E Y L A C L V L A M A L TCH200

 548 G W T N M L Y Y T R G F Q Q M G I Y A V M I E K M I L R D L C R F M F V Y I V F L F G F S T A V hVR1
 558 G W A N M L Y Y T R G F Q S M G M Y S V M I Q K V I L H D V L K F L F V Y I V F L L G F G V A L TCH200

 596 V T L I E D G K N D S L P S E S T S H R W R G P A C R P P D S S Y N S L Y S T C L E L F K F T I hVR1
 606 A S L I E K C P K D N - - - - - K D C - - - - - S S Y G S F S D A V L E L F K L T I TCH200

 644 G M G D L E P T E N Y D F K A V F I I L L L A Y V I L T Y I L L N M L I A L M G E T V N K I A hVR1
 638 G L G D L N I Q Q N S K Y P I L F L P L L I T Y V I L T F V L L N M L I A L M G E T V E N V S TCH200

 692 Q E S K N I W K L Q R A I T I L D T E K S F L K C M R K A F R S G K L L Q V G Y T P D G K D D Y hVR1
 686 K E S E R I W R L Q R A R T I L E F E K M L P E W L R S R F R M G E L C K V A - - - - - E D D F TCH200

 740 R W C F R V D E V N W T T W N T N V G I I N E D P G N C E G V K R T L S F S L R S S R V S G R H hVR1
 729 R L C L R I N E V K W T E W K T H V S F L N E D P G P - - - V R R T A D F N - - - - - TCH200

 788 W K N F A L V P L L R E A S A R D R Q S A Q P E E V Y L R Q F S G S L K P E D A E V F K S P A A hVR1
 764 - - - - - K I Q D S S R N N S K T T - - - L N A F - - - - - E E V E E F - - - P E TCH200

 836 S G E K hVR1
 789 T S V . TCH200

FIG. 14

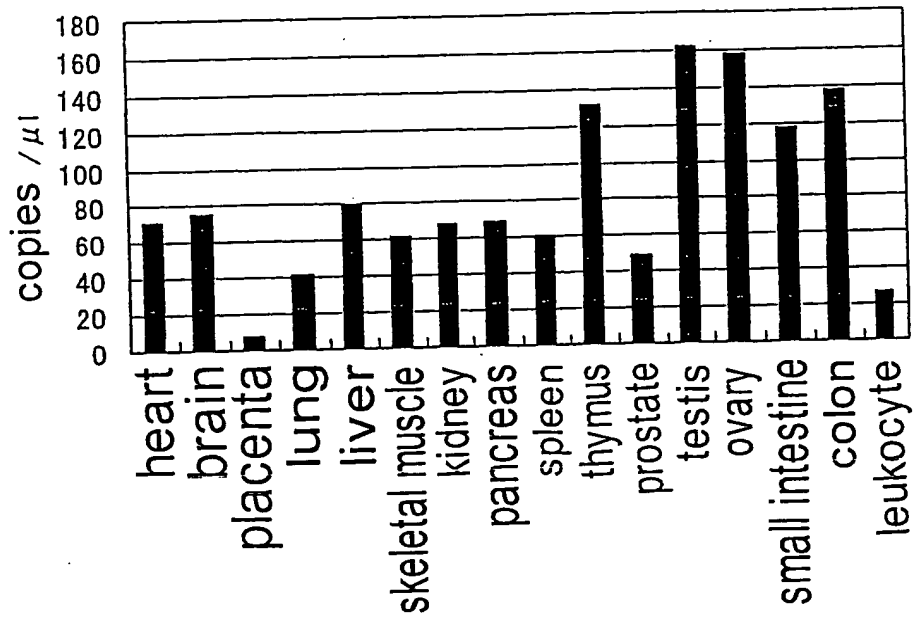


FIG. 15

1 M R A N C S S S S A C P A N S S E E E L P V G L E V H G N L E L V F T V V S T V hTCH230
 1 M S T D C A G N S T C P V N S T E E D P P V G M E G H A N L K L L F T V L S A V mTCH230
 41 M M G L L M F S L G C S V E I R K L W S H I R R P W G I A V G L L C Q F G L M P hTCH230
 41 M V G L V M F S F G C S V E S Q K L W L H L R R P W G I A V G L L S Q F G L M P mTCH230
 81 F T A Y L L A I S F S L K P V Q A I A V L I M G C C P G G T I S N I F T F W V D hTCH230
 81 L T A Y L L A I G F G L K P F Q A I A V L M M G S C P G G T I S N V L T F W V D mTCH230
 121 G D M D L S I S M T T C S T V A A L G M M P L C I Y L Y T W S W S L Q Q N L T I hTCH230
 121 G D M D L S I S M T T C S T V A A L G M M P L C L Y I Y T R S W T L T Q N L V I mTCH230
 161 P Y Q N I G I T L V C L T I P V A F G V Y V N Y R W P K Q S K I I L K I G A V V hTCH230
 161 P Y Q S I G I T L V S L V V P V A S G V Y V N Y R W P K Q A T V I L K V G A I L mTCH230
 201 G G V L L L V V A V A G V V L A K G S W N S D I T L L T I S F I F P L I G H V T hTCH230
 201 G G M L L L V V A V T G M V L A K G - W N T D V T L L V I S C I F P L V G H V T mTCH230
 241 G F L L A L F T H Q S W Q R C R T I S L E T G A Q N I Q M C I T M L Q L S F T A hTCH230
 240 G F L L A F L T H Q S W Q R C R T I S I E T G A Q N I Q L C I A M L Q L S F S A mTCH230
 281 E H L V Q M L S F P L A Y G L F Q L I D G F L I V A A Y Q T Y K R R L K N K H G hTCH230
 280 E Y L V Q L L N F A L A Y G L F Q V L H G L L I V A A Y Q A Y K R R Q K S K C R mTCH230
 321 K K N S G C T E V C H T R K S T S S R E T N A F L E V N E E G A I T P G P P G P hTCH230
 320 R Q H P D C P D V C Y E K Q P - - - R E T S A F L D K G D E A A V T L G P V Q P mTCH230
 361 M D C H R A L E P V G H I T S C E hTCH230
 357 E Q H H R A A E L T S H I P S C E mTCH230

FIG. 16

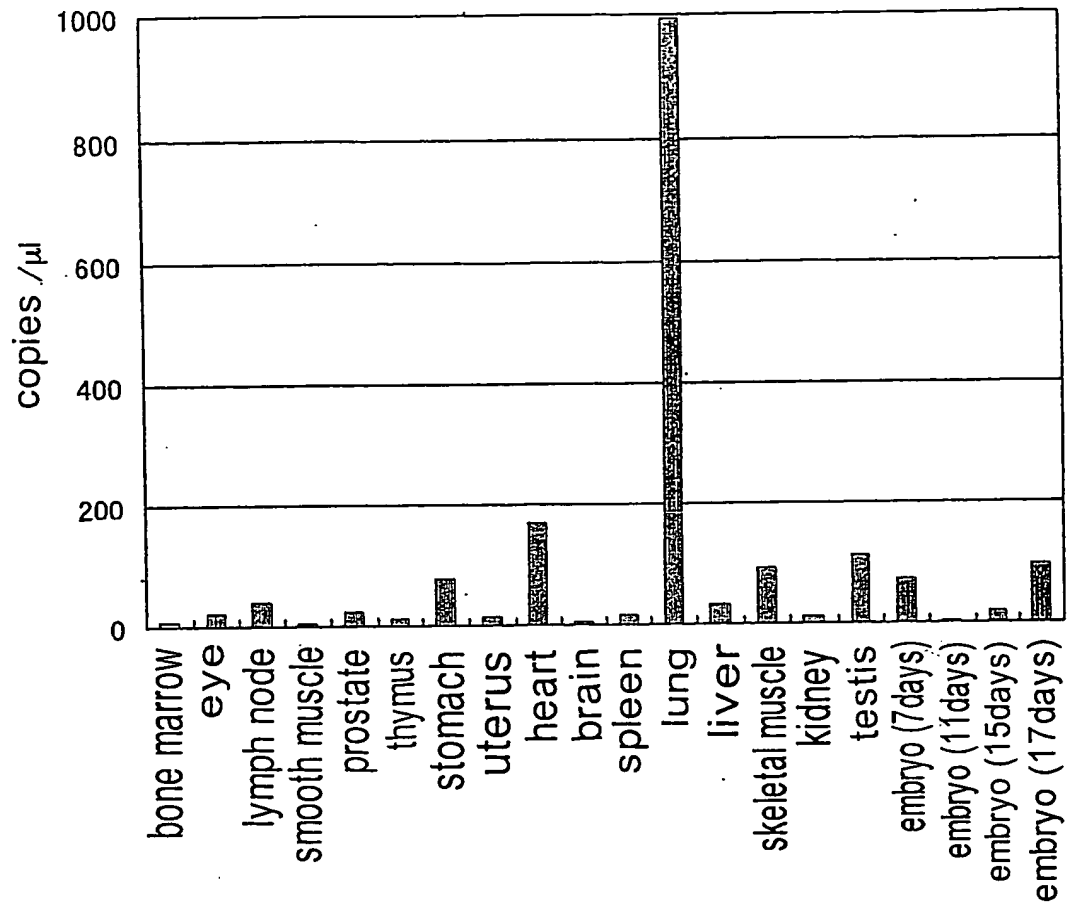


FIG. 17

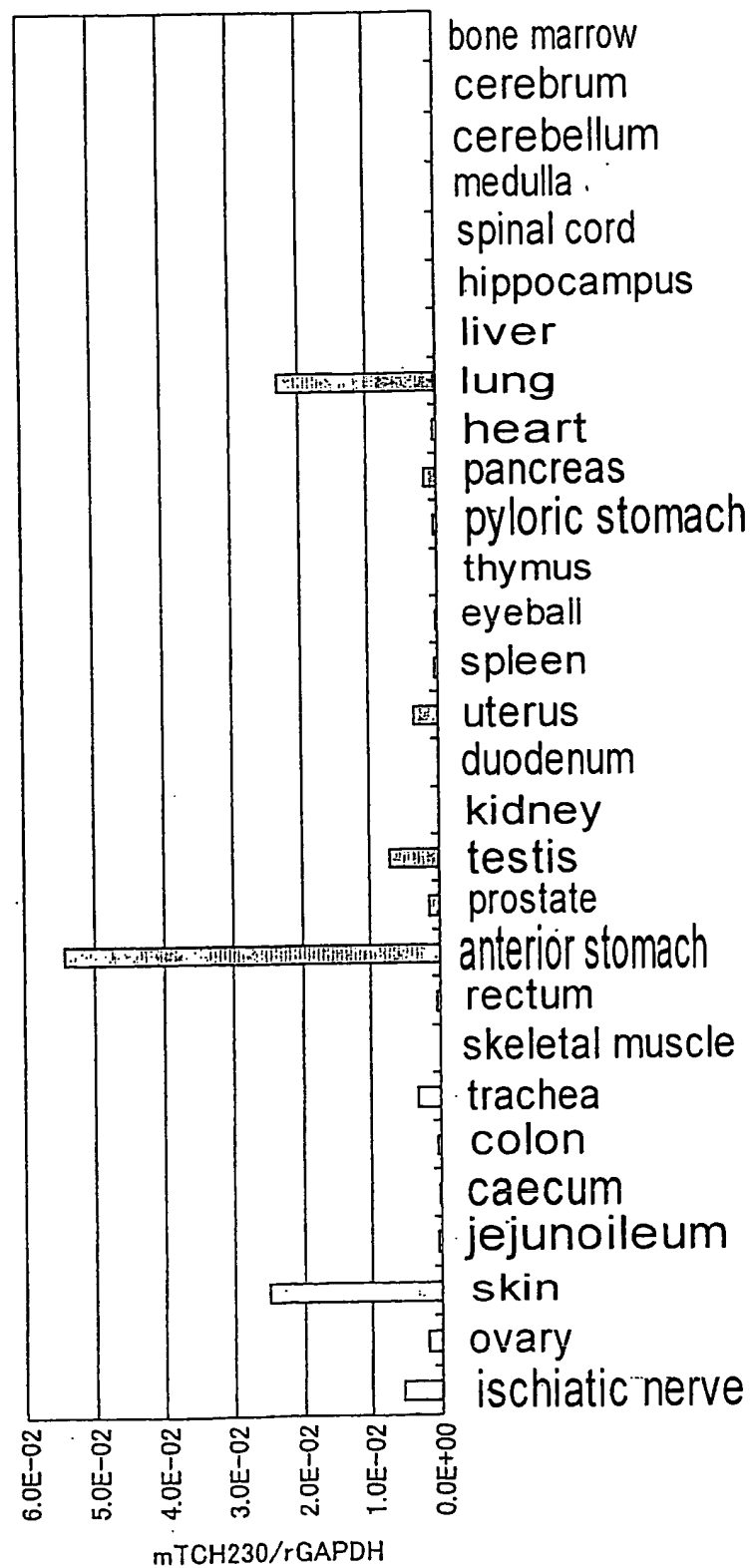


FIG. 18

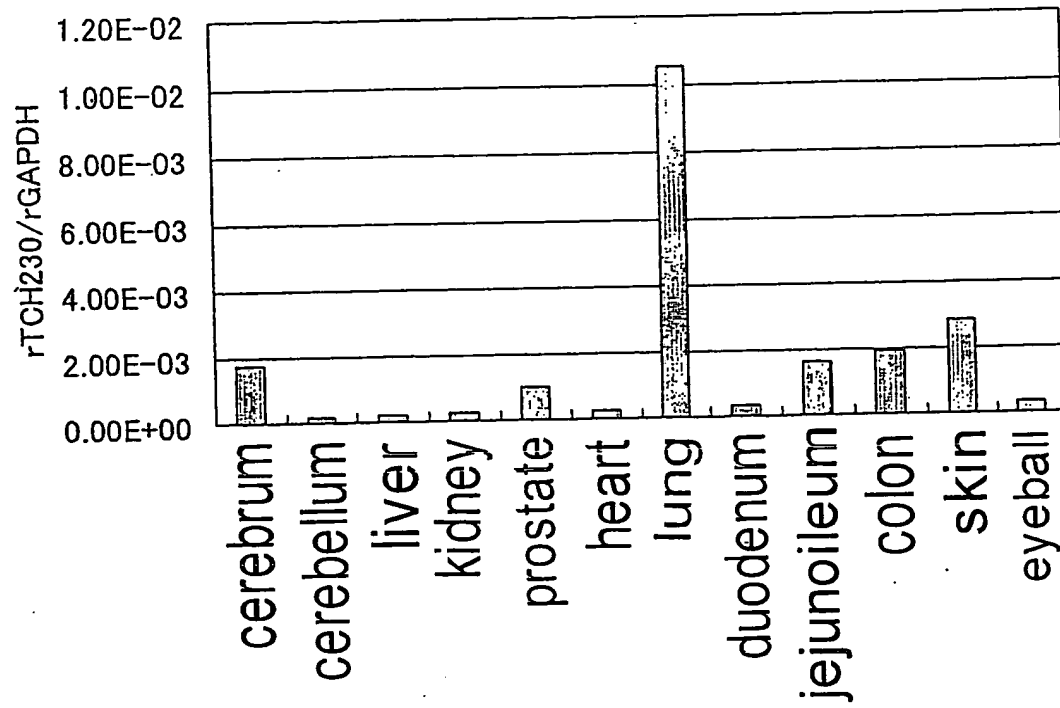


FIG. 19

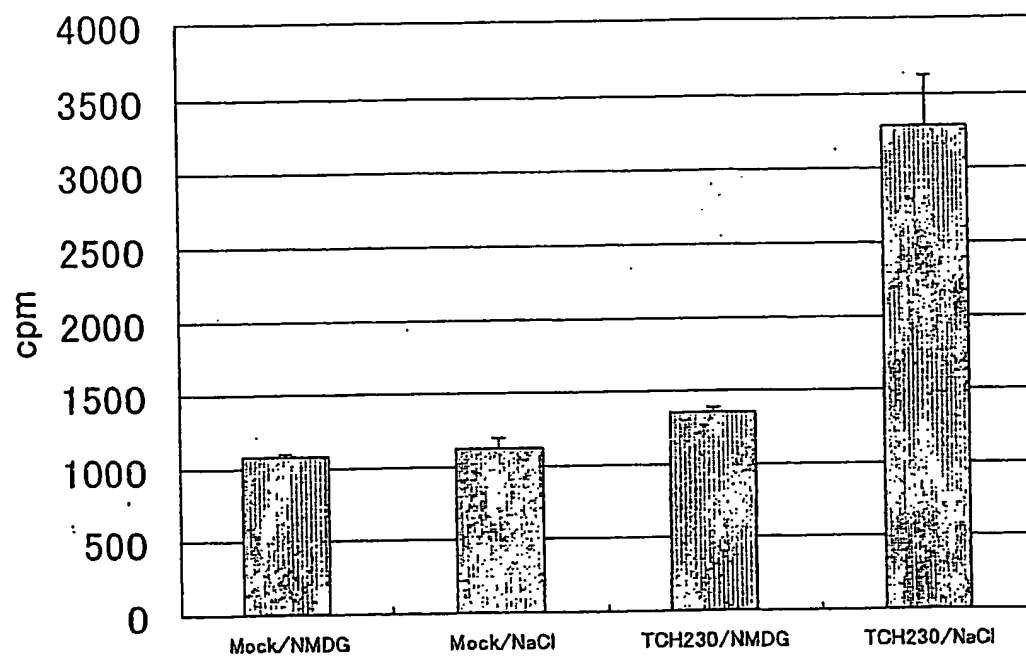


FIG. 20

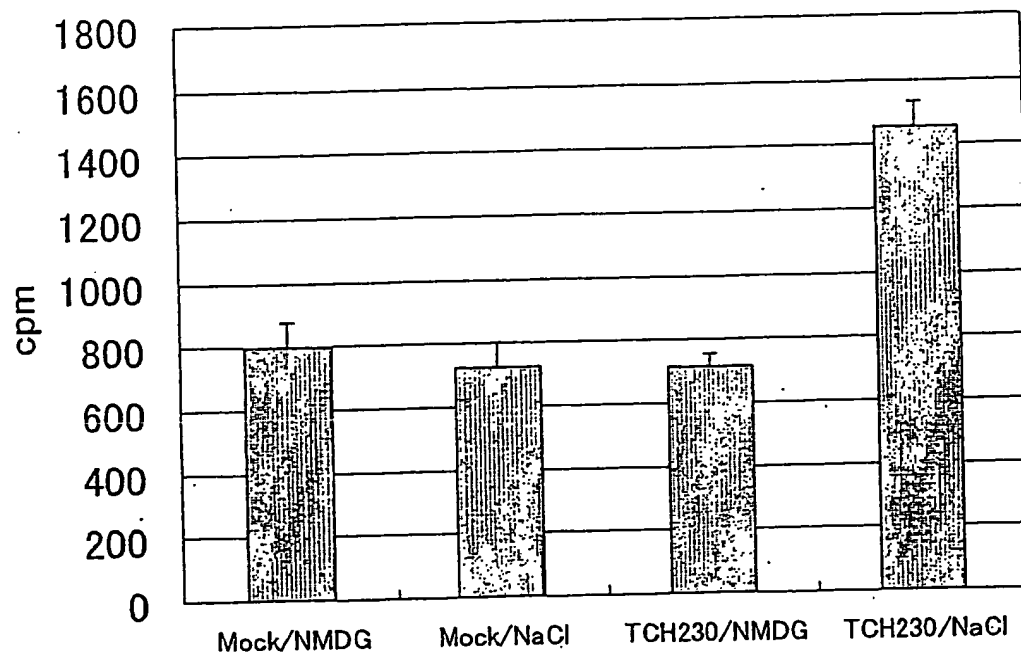


FIG. 21

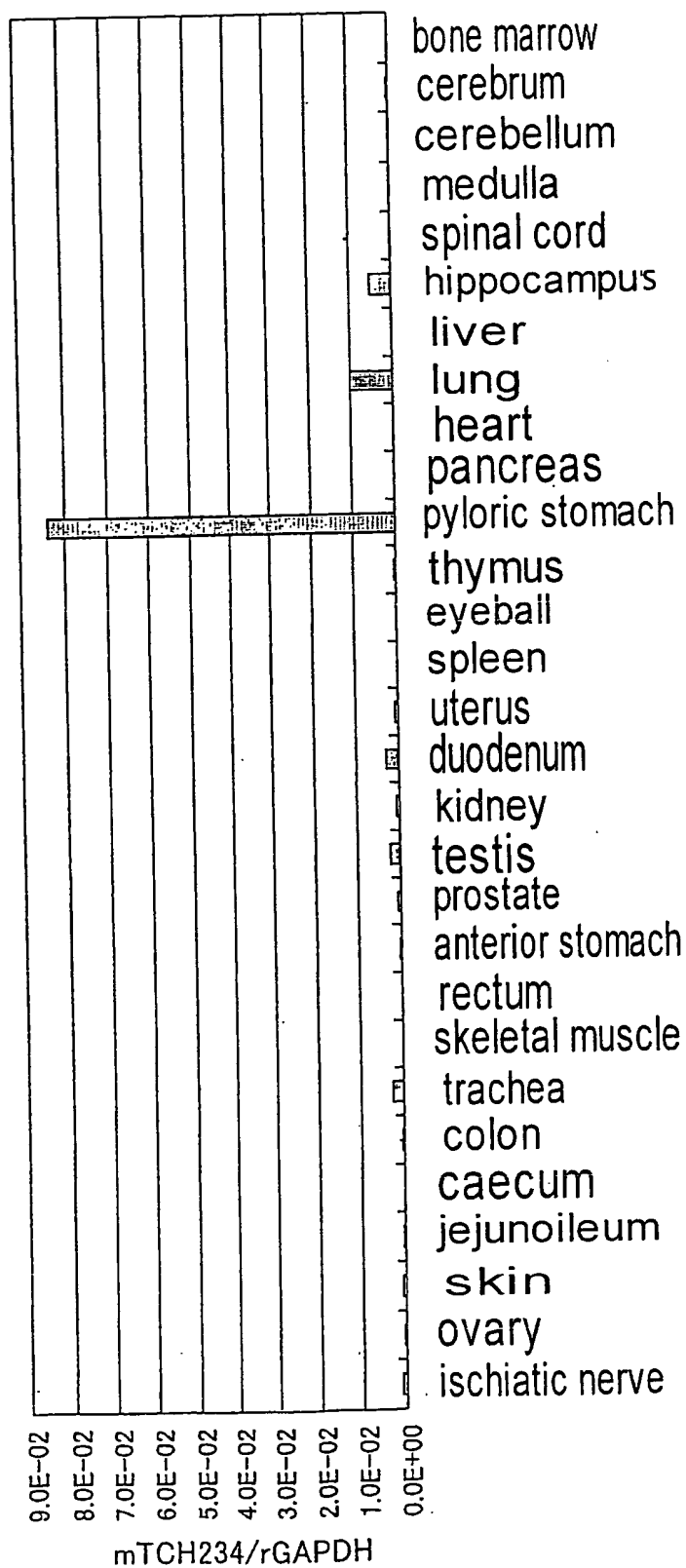


FIG. 22

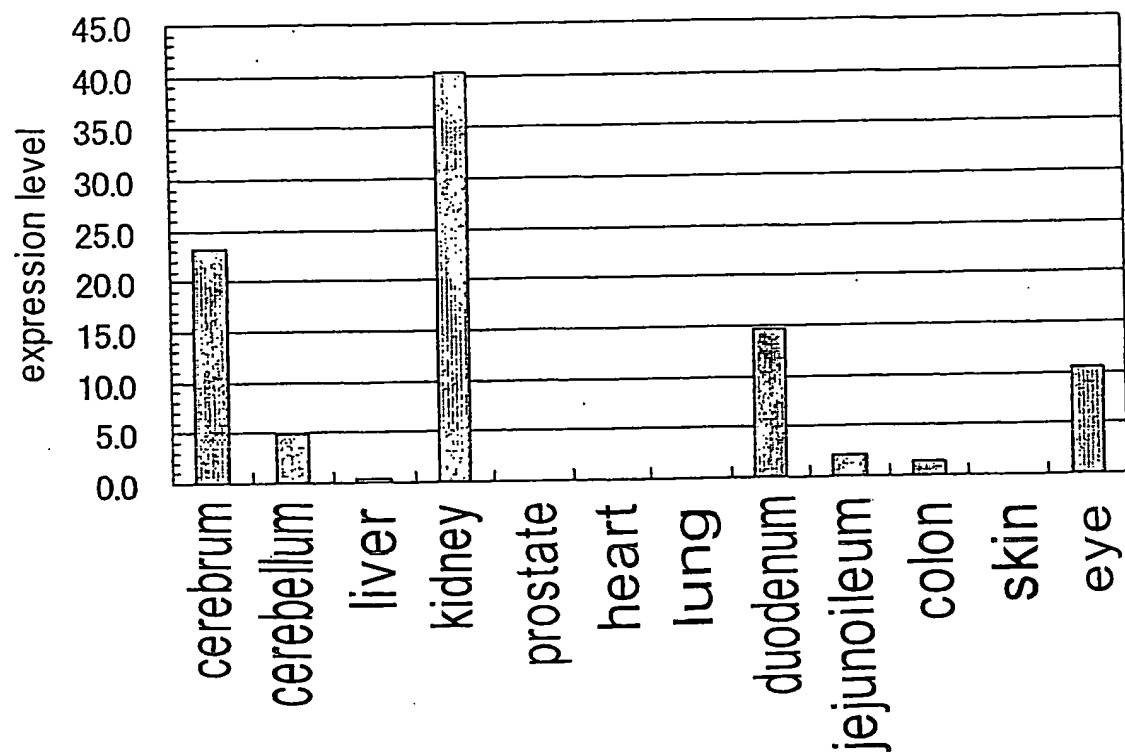


FIG. 23

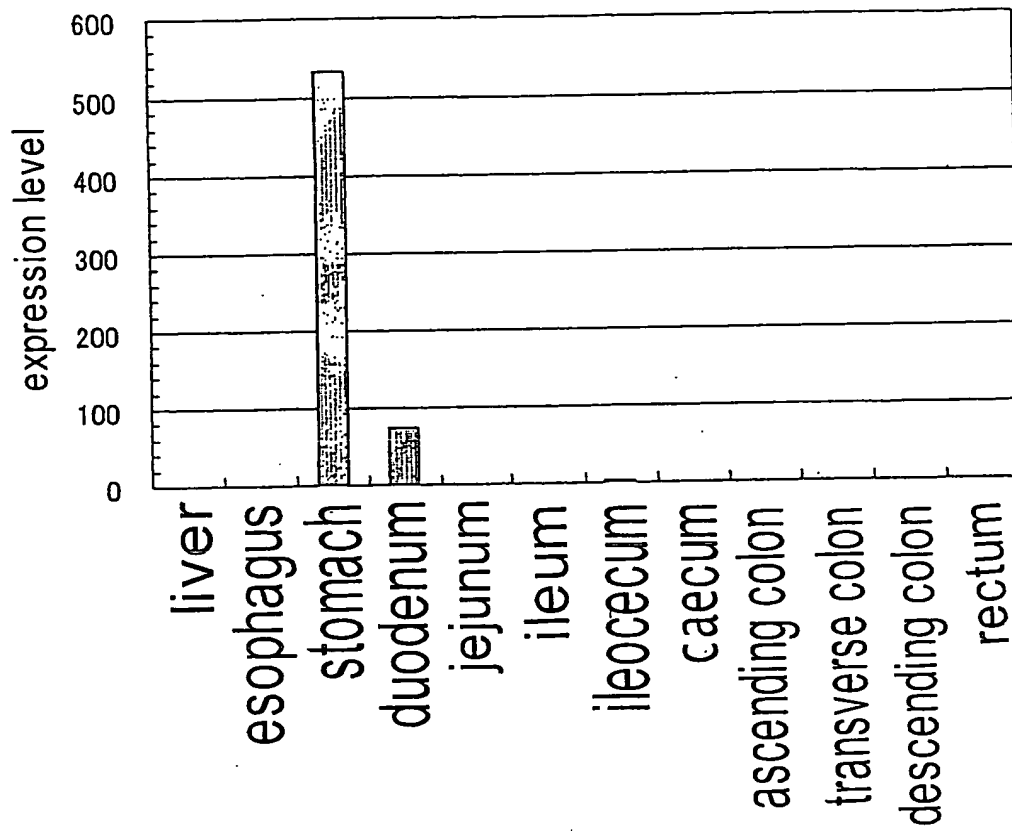


FIG. 24

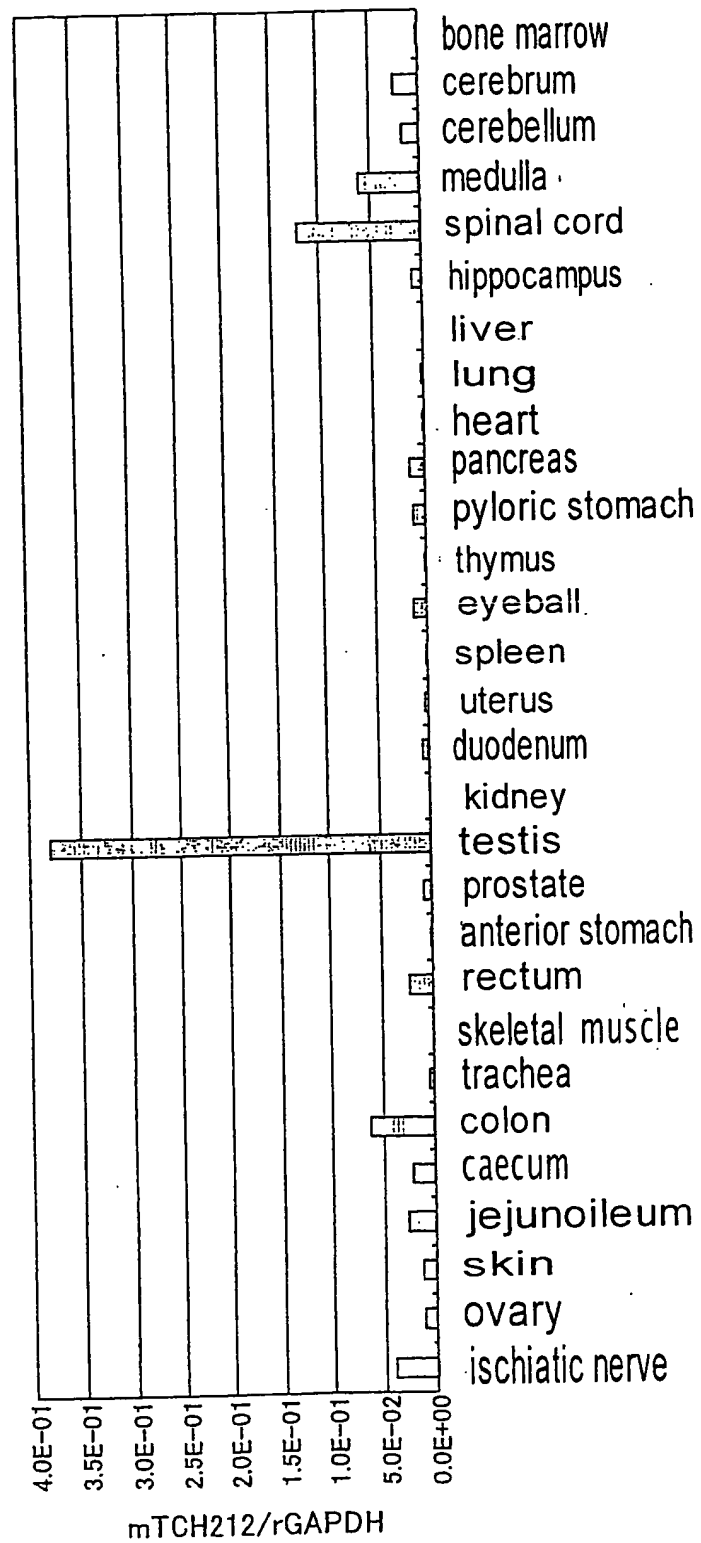


FIG. 25

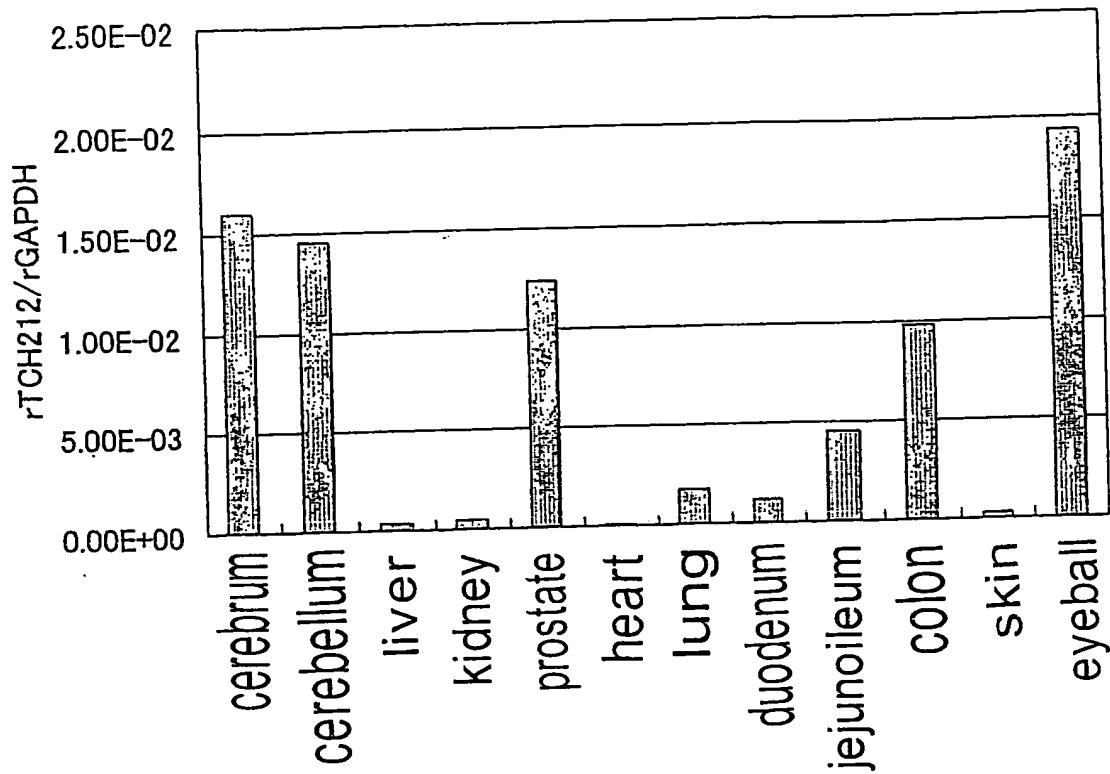


FIG. 26

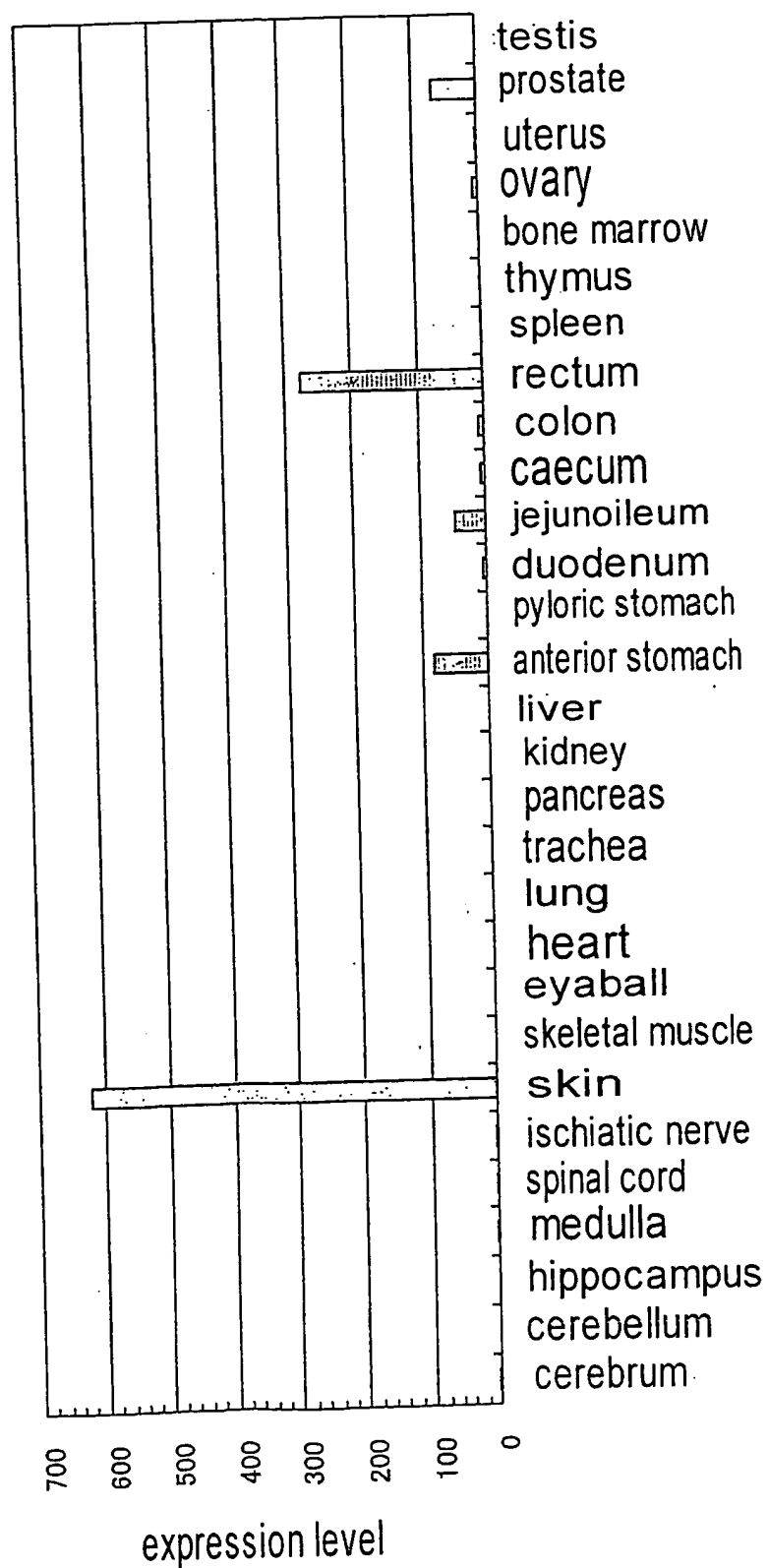


FIG. 27

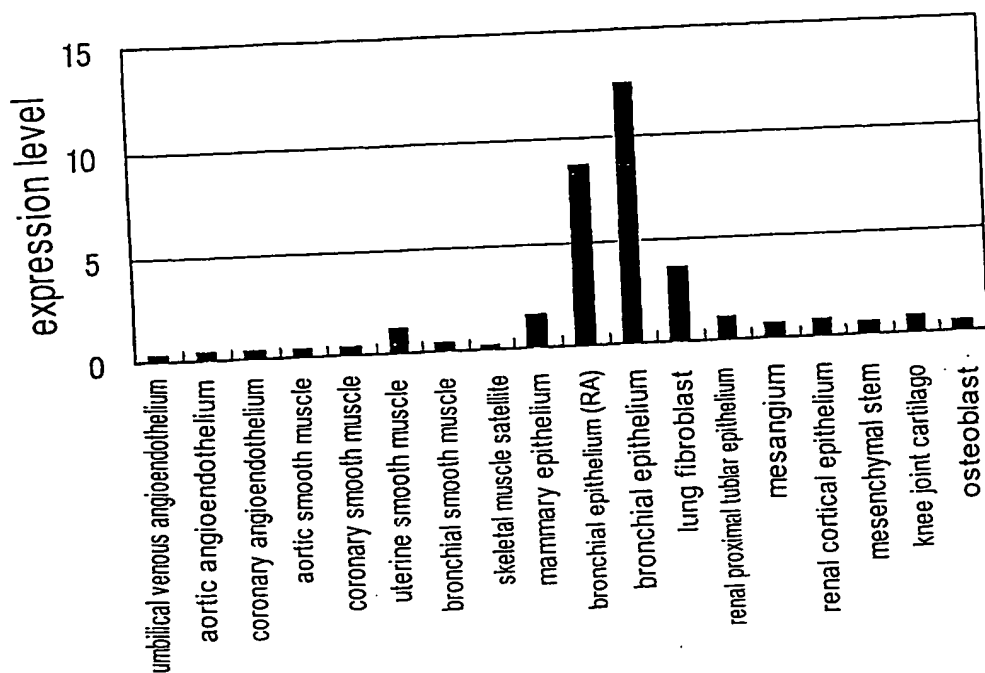


FIG. 28

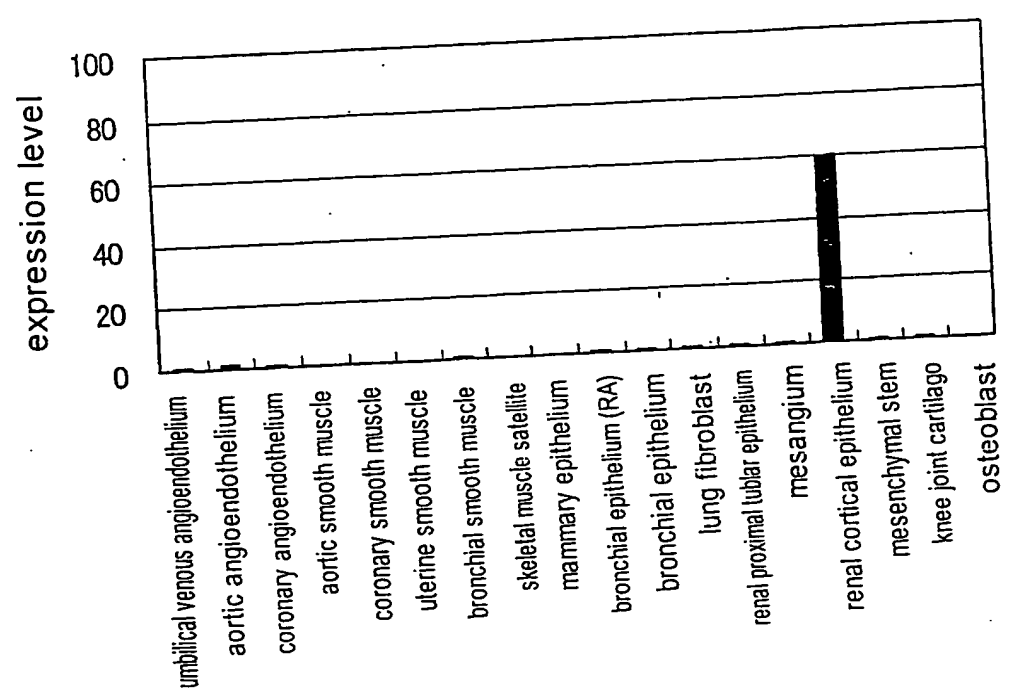


FIG. 29

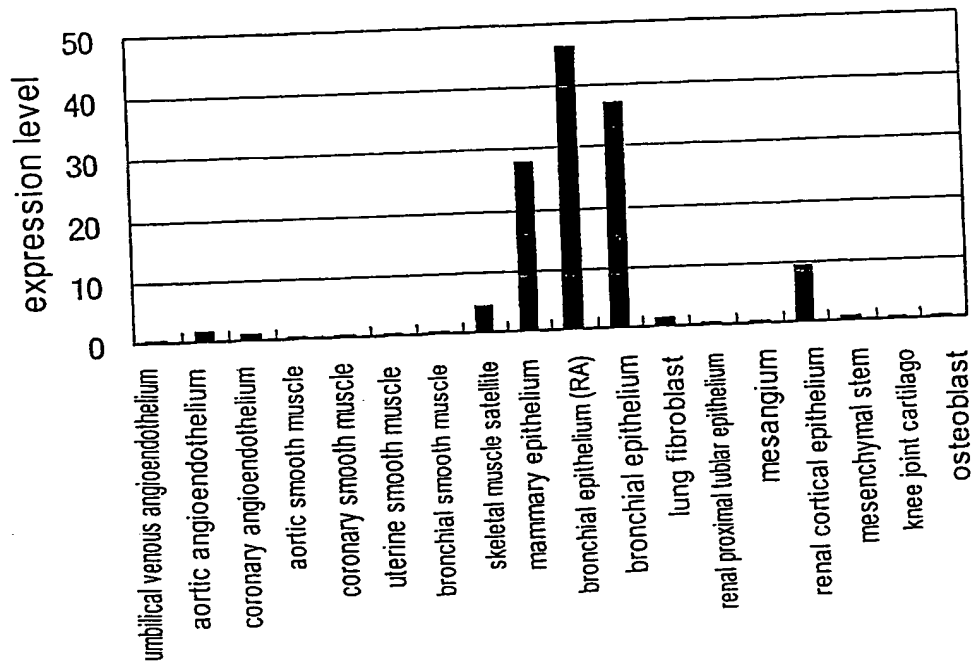


FIG. 30

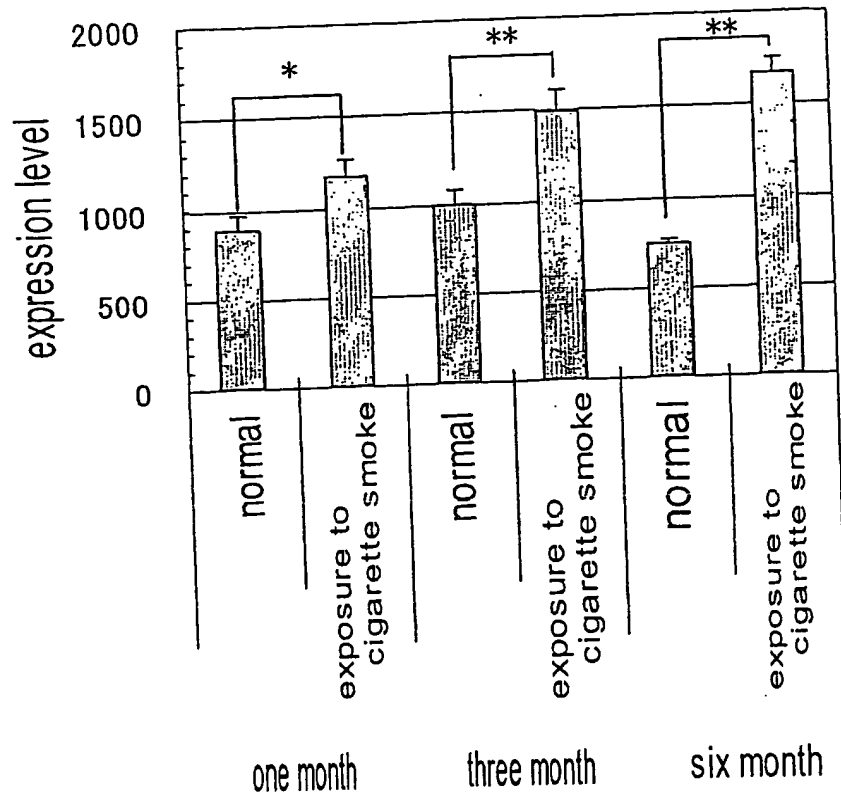


FIG. 31

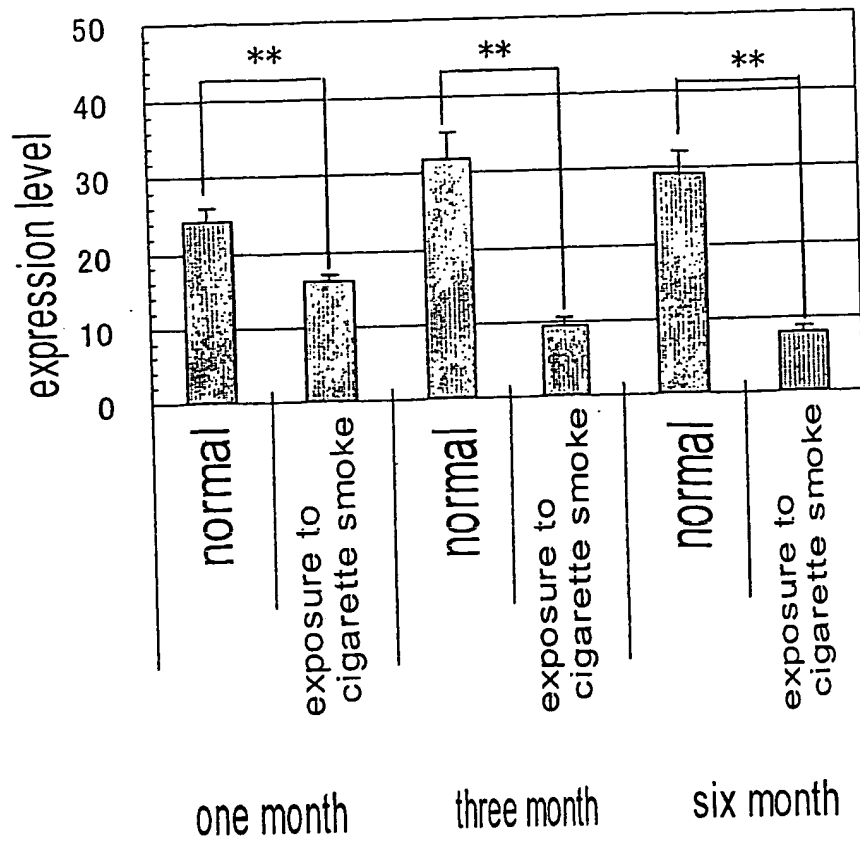


FIG. 32

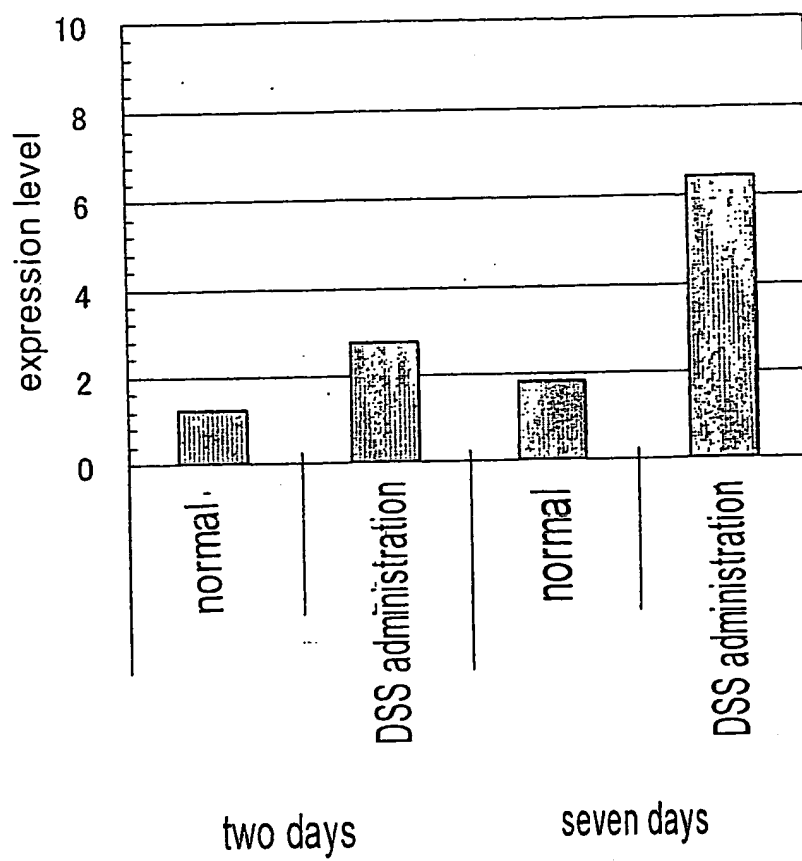


FIG. 33

